

Jason

List of Publications by Year in descending order

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37
papers

1,933
citations

471509

17
h-index

330143

37
g-index

37
all docs

37
docs citations

37
times ranked

2951
citing authors

#	ARTICLE	IF	CITATIONS
1	Yersinia pestis and the Plague of Justinian 541â€“543 AD: a genomic analysis. Lancet Infectious Diseases, The, 2014, 14, 319-326.	9.1	358
2	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. PeerJ, 2014, 2, e332.	2.0	265
3	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. Microbial Genomics, 2016, 2, e000074.	2.0	237
4	17th Century Variola Virus Reveals the Recent History of Smallpox. Current Biology, 2016, 26, 3407-3412.	3.9	197
5	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. Frontiers in Genetics, 2015, 6, 235.	2.3	160
6	Defining the Phylogenomics of Shigella Species: a Pathway to Diagnostics. Journal of Clinical Microbiology, 2015, 53, 951-960.	3.9	82
7	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. BMC Genomics, 2016, 17, 180.	2.8	71
8	More than 50% of Clostridium difficile Isolates from Pet Dogs in Flagstaff, USA, Carry Toxigenic Genotypes. PLoS ONE, 2016, 11, e0164504.	2.5	64
9	A Bacillus anthracis Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. MBio, 2016, 7, .	4.1	52
10	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. MBio, 2016, 7, .	4.1	49
11	Unprecedented Melioidosis Cases in Northern Australia Caused by an Asian Burkholderia pseudomallei Strain Identified by Using Large-Scale Comparative Genomics. Applied and Environmental Microbiology, 2016, 82, 954-963.	3.1	46
12	Burkholderia humptydoensis sp. nov., a New Species Related to Burkholderia thailandensis and the Fifth Member of the Burkholderia pseudomallei Complex. Applied and Environmental Microbiology, 2017, 83, .	3.1	45
13	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. Genome Medicine, 2015, 7, 52.	8.2	38
14	Population Structure and Genetic Diversity among Isolates of <i>Coccidioides posadasii</i> in Venezuela and Surrounding Regions. MBio, 2019, 10, .	4.1	28
15	Burkholderia pseudomallei, the causative agent of melioidosis, is rare but ecologically established and widely dispersed in the environment in Puerto Rico. PLoS Neglected Tropical Diseases, 2019, 13, e0007727.	3.0	26
16	Genomic Characterization of Burkholderia pseudomallei Isolates Selected for Medical Countermeasures Testing: Comparative Genomics Associated with Differential Virulence. PLoS ONE, 2015, 10, e0121052.	2.5	25
17	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of Clostridioides (Clostridium) difficile, despite cellular susceptibility to its toxins. Anaerobe, 2019, 58, 53-72.	2.1	20
18	Diverse Burkholderia Species Isolated from Soils in the Southern United States with No Evidence of B. pseudomallei. PLoS ONE, 2015, 10, e0143254.	2.5	20

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19	Reorganized Genomic Taxonomy of Francisellaceae Enables Design of Robust Environmental PCR Assays for Detection of <i>Francisella tularensis</i> . <i>Microorganisms</i> , 2021, 9, 146.	3.6	19
20	Differentiating Botulinum Neurotoxin-Producing Clostridia with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	18
21	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year <i>Burkholderia pseudomallei</i> infection. <i>PLoS Pathogens</i> , 2020, 16, e1008298.	4.7	12
22	Expanding the <i>Burkholderia pseudomallei</i> Complex with the Addition of Two Novel Species: <i>Burkholderia mayonis</i> sp. nov. and <i>Burkholderia savannae</i> sp. nov.. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0158321.	3.1	11
23	A chromosomal-level reference genome of the widely utilized <i>Coccidioides posadasii</i> laboratory strain "Silveira" G3: <i>Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	10
24	Selective whole genome amplification and sequencing of <i>Coxiella burnetii</i> directly from environmental samples. <i>Genomics</i> , 2020, 112, 1872-1878.	2.9	9
25	Whole-genome sequencing investigation of animal-skin-drum-associated UK anthrax cases reveals evidence of mixed populations and relatedness to a US case. <i>Microbial Genomics</i> , 2015, 1, e000039.	2.0	9
26	Genome Sequence of <i>Burkholderia pseudomallei</i> NCTC 13392. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
27	Evolutionary history and current distribution of the West Mediterranean lineage of <i>Brucella melitensis</i> in Italy. <i>Microbial Genomics</i> , 2020, 6, .	2.0	8
28	<i>Burkholderia ubonensis</i> Meropenem Resistance: Insights into Distinct Properties of Class A β -Lactamases in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Bacteria. <i>MBio</i> , 2020, 11, .	4.1	7
29	A global to local genomics analysis of <i>Clostridioides difficile</i> ST1/RT027 identifies cryptic transmission events in a northern Arizona healthcare network. <i>Microbial Genomics</i> , 2019, 5, .	2.0	7
30	Conservation of Resistance-Nodulation-Cell Division Efflux Pump-Mediated Antibiotic Resistance in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0092021.	3.2	6
31	Draft Genome Sequence of the First Pathogenic <i>Leptospira</i> Isolates from Ecuador. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
32	Developing Inclusivity and Exclusivity Panels for Testing Diagnostic and Detection Tools Targeting <i>Burkholderia pseudomallei</i> , the Causative Agent of Melioidosis. <i>Journal of AOAC INTERNATIONAL</i> , 2018, 101, 1920-1926.	1.5	5
33	<i>Burkholderia ubonensis</i> High-Level Tetracycline Resistance Is Due to Efflux Pump Synergy Involving a Novel TetA(64) Resistance Determinant. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	5
34	<i>Burkholderia pseudomallei</i> in Soil, US Virgin Islands, 2019. <i>Emerging Infectious Diseases</i> , 2020, 26, 2773-2775.	4.3	4
35	Complete Genome Sequence of <i>Peptacetobacter</i> (<i>Clostridium</i>) <i>hiranonis</i> Strain DGF055142, Isolated from Dog Feces from Flagstaff, Arizona, USA, 2019. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
36	Multiple phylogenetically-diverse, differentially-virulent <i>Burkholderia pseudomallei</i> isolated from a single soil sample collected in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010172.	3.0	3

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37	VNTR diversity in <i>Yersinia pestis</i> isolates from an animal challenge study reveals the potential for in vitro mutations during laboratory cultivation. <i>Infection, Genetics and Evolution</i> , 2016, 45, 297-302.	2.3	1